

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- Sub A6*
- (i) APPLICANT: NI, JIAN  
ROSEN, CRAIG A.  
PAN, JAMES G.  
GENTZ, REINER L.  
DIXIT, VISHVA M.
  - (ii) TITLE OF INVENTION: Death Domain Containing Receptor-4
  - (iii) NUMBER OF SEQUENCES: 11
  - (iv) CORRESPONDENCE ADDRESS:
    - (A) ADDRESSEE: HUMAN GENOME SCIENCES, INC.
    - (B) STREET: 9410 KEY WEST AVENUE
    - (C) CITY: ROCKVILLE
    - (D) STATE: MD
    - (E) COUNTRY: US
    - (F) ZIP: 20850
  - (v) COMPUTER READABLE FORM:
    - (A) MEDIUM TYPE: Floppy disk
    - (B) COMPUTER: IBM PC compatible
    - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
    - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
  - (vi) CURRENT APPLICATION DATA:
    - (A) APPLICATION NUMBER: US
    - (B) FILING DATE: 28-JAN-1997
    - (C) CLASSIFICATION:
  - (viii) ATTORNEY/AGENT INFORMATION:
    - (A) NAME: BROOKES, ANDERS A
    - (B) REGISTRATION NUMBER: 36,373
    - (C) REFERENCE/DOCKET NUMBER: PF355
  - (ix) TELECOMMUNICATION INFORMATION:
    - (A) TELEPHONE: (301) 309-8504
    - (B) TELEFAX: (301) 309-8512

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2152 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

00013895.012798

## (ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 19..1422

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTCGGGCACG	AGGGCAGG	ATG	GCG	CCA	CCA	CCA	GCT	AGA	GTA	CAT	CTA	GGT	51			
		Met	Ala	Pro	Pro	Pro	Ala	Arg	Val	His	Leu	Gly				
		1					5				10					
GCG	TTC	CTG	GCA	GTG	ACT	CCG	AAT	CCC	GGG	AGC	GCA	GCG	AGT	GGG	ACA	99
Ala	Phe	Leu	Ala	Val	Thr	Pro	Asn	Pro	Gly	Ser	Ala	Ala	Ser	Gly	Thr	
		15					20						25			
GAG	GCA	GCC	GCG	GCC	ACA	CCC	AGC	AAA	GTG	TGG	GGC	TCT	TCC	GCG	GGG	147
Glu	Ala	Ala	Ala	Ala	Thr	Pro	Ser	Lys	Val	Trp	Gly	Ser	Ser	Ala	Gly	
		30					35					40				
AGG	ATT	GAA	CCA	CGA	GGC	GGG	GGC	CGA	GGA	GCG	CTC	CCT	ACC	TCC	ATG	195
Arg	Ile	Glu	Pro	Arg	Gly	Gly	Gly	Arg	Gly	Ala	Leu	Pro	Thr	Ser	Met	
	45					50					55					
GGA	CAG	CAC	GGA	CCC	AGT	GCC	CGG	GCC	CGG	GCA	GGG	CGC	GCC	CCA	GGA	243
Gly	Gln	His	Gly	Pro	Ser	Ala	Arg	Ala	Arg	Ala	Gly	Arg	Ala	Pro	Gly	
	60				65				70						75	
CCC	AGG	CCG	GCG	CGG	GAA	GCC	AGC	CCT	CGG	CTC	CGG	GTC	CAC	AAG	ACC	291
Pro	Arg	Pro	Ala	Arg	Glu	Ala	Ser	Pro	Arg	Leu	Arg	Val	His	Lys	Thr	
			80					85						90		
TTC	AAG	TTT	GTC	GTC	GTC	GGG	GTC	CTG	CTG	CAG	GTC	GTA	CCT	AGC	TCA	339
Phe	Lys	Phe	Val	Val	Val	Gly	Val	Leu	Leu	Gln	Val	Val	Pro	Ser	Ser	
			95					100					105			
GCT	GCA	ACC	ATC	AAA	CTT	CAT	GAT	CAA	TCA	ATT	GGC	ACA	CAG	CAA	TGG	387
Ala	Ala	Thr	Ile	Lys	Leu	His	Asp	Gln	Ser	Ile	Gly	Thr	Gln	Gln	Trp	
		110					115					120				
GAA	CAT	AGC	CCT	TTG	GGA	GAG	TTG	TGT	CCA	CCA	GGA	TCT	CAT	AGA	TCA	435
Glu	His	Ser	Pro	Leu	Gly	Glu	Leu	Cys	Pro	Pro	Gly	Ser	His	Arg	Ser	
	125					130					135					
GAA	CGT	CCT	GGA	GCC	TGT	AAC	CGG	TGC	ACA	GAG	GGT	GTG	GGT	TAC	ACC	483
Glu	Arg	Pro	Gly	Ala	Cys	Asn	Arg	Cys	Thr	Glu	Gly	Val	Gly	Tyr	Thr	
	140				145					150					155	
AAT	GCT	TCC	AAC	AAT	TTG	TTT	GCT	TGC	CTC	CCA	TGT	ACA	GCT	TGT	AAA	531
Asn	Ala	Ser	Asn	Asn	Leu	Phe	Ala	Cys	Leu	Pro	Cys	Thr	Ala	Cys	Lys	
			160					165						170		
TCA	GAT	GAA	GAA	GAG	AGA	AGT	CCC	TGC	ACC	ACG	ACC	AGG	AAC	ACA	GCA	579
Ser	Asp	Glu	Glu	Glu	Arg	Ser	Pro	Cys	Thr	Thr	Thr	Arg	Asn	Thr	Ala	
		175						180					185			

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TGT CAG TGC AAA CCA GGA ACT TTC CGG AAT GAC AAT TCT GCT GAG ATG	627
Cys Gln Cys Lys Pro Gly Thr Phe Arg Asn Asp Asn Ser Ala Glu Met	
190 195 200	
TGC CGG AAG TGC AGC ACA GGG TGC CCC AGA GGG ATG GTC AAG GTC AAG	675
Cys Arg Lys Cys Ser Thr Gly Cys Pro Arg Gly Met Val Lys Val Lys	
205 210 215	
GAT TGT ACG CCC TGG AGT GAC ATC GAG TGT GTC CAC AAA GAA TCA GGC	723
Asp Cys Thr Pro Trp Ser Asp Ile Glu Cys Val His Lys Glu Ser Gly	
220 225 230 235	
AAT GGA CAT AAT ATA TGG GTG ATT TTG GTT GTG ACT TTG GTT GTT CCG	771
Asn Gly His Asn Ile Trp Val Ile Leu Val Val Thr Leu Val Val Pro	
240 245 250	
TTG CTG TTG GTG GCT GTG CTG ATT GTC TGT TGT TGC ATC GGC TCA GGT	819
Leu Leu Leu Val Ala Val Leu Ile Val Cys Cys Cys Ile Gly Ser Gly	
255 260 265	
TGT GGA GGG GAC CCC AAG TGC ATG GAC AGG GTG TGT TTC TGG CGC TTG	867
Cys Gly Gly Asp Pro Lys Cys Met Asp Arg Val Cys Phe Trp Arg Leu	
270 275 280	
GGT CTC CTA CGA GGG CCT GGG GCT GAG GAC AAT GCT CAC AAC GAG ATT	915
Gly Leu Leu Arg Gly Pro Gly Ala Glu Asp Asn Ala His Asn Glu Ile	
285 290 295	
CTG AGC AAC GCA GAC TCG CTG TCC ACT TTC GTC TCT GAG CAG CAA ATG	963
Leu Ser Asn Ala Asp Ser Leu Ser Thr Phe Val Ser Glu Gln Gln Met	
300 305 310 315	
GAA AGC CAG GAG CCG GCA GAT TTG ACA GGT GTC ACT GTA CAG TCC CCA	1011
Glu Ser Gln Glu Pro Ala Asp Leu Thr Gly Val Thr Val Gln Ser Pro	
320 325 330	
GGG GAG GCA CAG TGT CTG CTG GGA CCG GCA GAA GCT GAA GGG TCT CAG	1059
Gly Glu Ala Gln Cys Leu Leu Gly Pro Ala Glu Ala Glu Gly Ser Gln	
335 340 345	
AGG AGG AGG CTG CTG GTT CCA GCA AAT GGT GCT GAC CCC ACT GAG ACT	1107
Arg Arg Arg Leu Leu Val Pro Ala Asn Gly Ala Asp Pro Thr Glu Thr	
350 355 360	
CTG ATG CTG TTC TTT GAC AAG TTT GCA AAC ATC GTG CCC TTT GAC TCC	1155
Leu Met Leu Phe Phe Asp Lys Phe Ala Asn Ile Val Pro Phe Asp Ser	
365 370 375	
TGG GAC CAG CTC ATG AGG CAG CTG GAC CTC ACG AAA AAT GAG ATC GAT	1203
Trp Asp Gln Leu Met Arg Gln Leu Asp Leu Thr Lys Asn Glu Ile Asp	
380 385 390 395	
GTG GTC AGA GCT GGT ACA GCA GGC CCA GGG GAT GCC TTG TAT GCA ATG	1251
Val Val Arg Ala Gly Thr Ala Gly Pro Gly Asp Ala Leu Tyr Ala Met	

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400	405	410	
CTG ATG AAA TGG GTC AAC AAA ACT	GGA CGG AAC GCC TCG ATC CAC ACC		1299
Leu Met Lys Trp Val Asn Lys Thr	Gly Arg Asn Ala Ser Ile His Thr		
415	420	425	
CTG CTG GAT GCC TTG GAG AGG ATG	GAA GAG AGA CAT GCA AAA GAG AAG		1347
Leu Leu Asp Ala Leu Glu Arg Met	Glu Glu Arg His Ala Lys Glu Lys		
430	435	440	
ATT CAG GAC CTC TTG GTG GAC TCT	GGA AAG TTC ATC TAC TTA GAA GAT		1395
Ile Gln Asp Leu Leu Val Asp Ser	Gly Lys Phe Ile Tyr Leu Glu Asp		
445	450	455	
GGC ACA GGC TCT GCC GTG TCC TTG	GAG TGAAAGACTC TTTTACCAG		1442
Gly Thr Gly Ser Ala Val Ser Leu Glu			
460	465		
AGGTTTCCTC TTAGGTGTTA GGAGTTAATA	CATATTAGGT TTTTTTTTTT TTTAACATGT		1502
ATACAAAGTA AATTCTTAGC CACGTGTATT	GGCTCCTGCC TGTAATCCCA TCACTTTGGG		1562
AGGCTGACGC CGGTGGATCC ACTTGAGGTC	CGAAGTTCCA AGACCAGCCC TGAACCAACA		1622
TCGTGGAAAT GCCCGTCTTT TACAAAAAAA	TACCAAAAAT TCAACTGGAA TGTGCATGGT		1682
GTGTGCCATC ATTTCTCGG CTAACACGG	GAGGTCTGAG GCCAGGAGAA TCCACTTGAA		1742
CCCCACGAAG GACAGTGTAG ACTGCAGATT	GCACCACTGC ACTCCCAGCC TGGGAACACA		1802
GAGCAAGACT CTGTCTCAAG ATAAAATAAA	ATAAACTTGA AAGAATTATT GCCCGACTGA		1862
GGCTCACATG CCAAAGGAAA ATCTGGTTCT	CCCCTGAGCT GGCCTCCGTG TGTTCCTTA		1922
TCATGGTGGT CAATTGGAGG TGTTAATTTG	AATGGATTAA GGAACACCTA GAACACTGGT		1982
AAGGCATTAT TTCTGGGACA TTATTTCTGG	GCATGTCTTC GAGGGTGTTT CCAGAGGGGA		2042
TTGGCATGCG ATCGGGTGGA CTGAGTGGA	AAGACCTACG CTTAATTTGG GGGGGCACCG		2102
TCCGACAGAC TGGGGAGCAA GATAGAAGAA	AACAAAAAAA AAAAAAAAAA		2152

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Pro Pro Pro Ala Arg Val His Leu Gly Ala Phe Leu Ala Val

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Sub  
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Cont.

1	5	10	15
Thr Pro Asn	Pro Gly Ser Ala Ala	Ser Gly Thr Glu Ala Ala Ala	Ala Ala
	20	25	30
Thr Pro Ser	Lys Val Trp Gly Ser Ser Ala Gly Arg Ile Glu Pro Arg		
	35	40	45
Gly Gly Gly Arg	Gly Ala Leu Pro Thr Ser Met Gly Gln His Gly Pro		
	50	55	60
Ser Ala Arg Ala Arg	Ala Gly Arg Ala Pro Gly Pro Arg Pro Ala Arg		
	65	70	75
Glu Ala Ser Pro Arg	Leu Arg Val His Lys Thr Phe Lys Phe Val Val		
	85	90	95
Val Gly Val Leu Leu Gln Val Val	Pro Ser Ser Ala Ala Thr Ile Lys		
	100	105	110
Leu His Asp Gln Ser Ile Gly Thr Gln Gln Trp Glu His Ser Pro Leu			
	115	120	125
Gly Glu Leu Cys Pro Pro Gly Ser His Arg Ser Glu Arg Pro Gly Ala			
	130	135	140
Cys Asn Arg Cys Thr Glu Gly Val Gly Tyr Thr Asn Ala Ser Asn Asn			
	145	150	155
Leu Phe Ala Cys Leu Pro Cys Thr Ala Cys Lys Ser Asp Glu Glu Glu			
	165	170	175
Arg Ser Pro Cys Thr Thr Thr Arg Asn Thr Ala Cys Gln Cys Lys Pro			
	180	185	190
Gly Thr Phe Arg Asn Asp Asn Ser Ala Glu Met Cys Arg Lys Cys Ser			
	195	200	205
Thr Gly Cys Pro Arg Gly Met Val Lys Val Lys Asp Cys Thr Pro Trp			
	210	215	220
Ser Asp Ile Glu Cys Val His Lys Glu Ser Gly Asn Gly His Asn Ile			
	225	230	235
Trp Val Ile Leu Val Val Thr Leu Val Val Pro Leu Leu Leu Val Ala			
	245	250	255
Val Leu Ile Val Cys Cys Cys Ile Gly Ser Gly Cys Gly Gly Asp Pro			
	260	265	270
Lys Cys Met Asp Arg Val Cys Phe Trp Arg Leu Gly Leu Leu Arg Gly			
	275	280	285
Pro Gly Ala Glu Asp Asn Ala His Asn Glu Ile Leu Ser Asn Ala Asp			
	290	295	300

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Sub  
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Cont.

Ser Leu Ser Thr Phe Val Ser Glu Gln Gln Met Glu Ser Gln Glu Pro  
 305 310 315 320  
 Ala Asp Leu Thr Gly Val Thr Val Gln Ser Pro Gly Glu Ala Gln Cys  
 325 330 335  
 Leu Leu Gly Pro Ala Glu Ala Glu Gly Ser Gln Arg Arg Arg Leu Leu  
 340 345 350  
 Val Pro Ala Asn Gly Ala Asp Pro Thr Glu Thr Leu Met Leu Phe Phe  
 355 360 365  
 Asp Lys Phe Ala Asn Ile Val Pro Phe Asp Ser Trp Asp Gln Leu Met  
 370 375 380  
 Arg Gln Leu Asp Leu Thr Lys Asn Glu Ile Asp Val Val Arg Ala Gly  
 385 390 395 400  
 Thr Ala Gly Pro Gly Asp Ala Leu Tyr Ala Met Leu Met Lys Trp Val  
 405 410 415  
 Asn Lys Thr Gly Arg Asn Ala Ser Ile His Thr Leu Leu Asp Ala Leu  
 420 425 430  
 Glu Arg Met Glu Glu Arg His Ala Lys Glu Lys Ile Gln Asp Leu Leu  
 435 440 445  
 Val Asp Ser Gly Lys Phe Ile Tyr Leu Glu Asp Gly Thr Gly Ser Ala  
 450 455 460  
 Val Ser Leu Glu  
 465

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 669 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Leu Gly Ile Trp Thr Leu Leu Pro Leu Val Leu Thr Ser Val Ala  
 1 5 10 15  
 Arg Leu Ser Ser Lys Ser Val Asn Ala Gln Val Thr Asp Ile Asn Ser  
 20 25 30

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Lys Gly Leu Glu Leu Arg Lys Thr Val Thr Thr Val Glu Thr Gln Asn  
 35 40 45  
 Leu Glu Gly Leu His His Asp Gly Gln Phe Cys His Lys Pro Cys Pro  
 50 55 60  
 Pro Gly Glu Arg Lys Ala Arg Asp Cys Thr Val Asn Gly Asp Glu Pro  
 65 70 75 80  
 Asp Cys Val Pro Cys Gln Glu Gly Lys Glu Tyr Thr Asp Lys Ala His  
 85 90 95  
 Phe Ser Ser Lys Cys Arg Arg Cys Arg Leu Cys Asp Glu Gly His Gly  
 100 105 110  
 Leu Glu Val Glu Ile Asn Cys Thr Arg Thr Gln Asn Thr Lys Cys Arg  
 115 120 125  
 Cys Lys Pro Asn Phe Phe Cys Asn Ser Thr Val Cys Glu His Cys Asp  
 130 135 140  
 Pro Cys Thr Lys Cys Glu His Gly Ile Ile Lys Glu Cys Thr Leu Thr  
 145 150 155 160  
 Ser Asn Thr Lys Cys Lys Glu Glu Gly Ser Arg Ser Asn Leu Gly Trp  
 165 170 175  
 Leu Cys Leu Leu Leu Leu Pro Ile Pro Leu Ile Val Trp Val Lys Arg  
 180 185 190  
 Lys Glu Val Gln Lys Thr Cys Arg Lys His Arg Lys Glu Asn Gln Gly  
 195 200 205  
 Ser His Glu Ser Pro Thr Leu Asn Pro Glu Thr Val Ala Ile Asn Leu  
 210 215 220  
 Ser Asp Val Asp Leu Ser Lys Tyr Ile Thr Thr Ile Ala Gly Val Met  
 225 230 235 240  
 Thr Leu Ser Gln Val Lys Gly Phe Val Arg Lys Asn Gly Val Asn Glu  
 245 250 255  
 Ala Lys Ile Asp Glu Ile Lys Asn Asp Asn Val Gln Asp Thr Ala Glu  
 260 265 270  
 Gln Lys Val Gln Leu Leu Arg Asn Trp His Gln Leu His Gly Lys Lys  
 275 280 285  
 Glu Ala Tyr Asp Thr Leu Ile Lys Asp Leu Lys Lys Ala Asn Leu Cys  
 290 295 300  
 Thr Leu Ala Glu Lys Ile Gln Thr Ile Ile Leu Lys Asp Ile Thr Ser  
 305 310 315 320  
 Asp Ser Glu Asn Ser Asn Phe Arg Asn Glu Ile Gln Ser Leu Val Met

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Sub  
A6  
Cont-

335

Sub  
A6  
cont



Tyr Asp Thr Leu Ile Lys Asp Leu Lys Lys Ala Asn Leu Cys Thr Leu  
625 630 635 640

Ala Glu Lys Ile Gln Thr Ile Ile Leu Lys Asp Ile Thr Ser Asp Ser  
645 650 655

Glu Asn Ser Asn Phe Arg Asn Glu Ile Gln Ser Leu Val  
660 665

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 909 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Gly Leu Ser Thr Val Pro Asp Leu Leu Pro Leu Val Leu Leu Glu  
1 5 10 15

Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro His  
20 25 30

Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys Tyr  
35 40 45

Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys Gly  
50 55 60

Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Asp Thr Asp Cys Arg  
65 70 75 80

Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu Arg His  
85 90 95

Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile  
100 105 110

Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn  
115 120 125

Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys  
130 135 140

Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln  
145 150 155 160

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Sub  
A6  
Cont.

Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu  
 165 170 175  
 Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu  
 180 185 190  
 Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser Gly Thr  
 195 200 205  
 Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu Leu Ser  
 210 215 220  
 Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys Ser Lys  
 225 230 235 240  
 Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu Gly Glu  
 245 250 255  
 Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser Phe Ser  
 260 265 270  
 Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val Pro Ser  
 275 280 285  
 Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys Pro Asn  
 290 295 300  
 Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly Ala Asp  
 305 310 315 320  
 Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn Pro Leu  
 325 330 335  
 Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp Thr Asp  
 340 345 350  
 Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro Leu Arg  
 355 360 365  
 Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu Ile Asp  
 370 375 380  
 Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln Tyr Ser  
 385 390 395 400  
 Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala Thr Leu  
 405 410 415  
 Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly Cys Leu  
 420 425 430  
 Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro Pro Ala  
 435 440 445  
 Pro Ser Leu Leu Arg Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu

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Sub  
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Cont.

450		455		460
Pro Leu Val Leu Leu Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val				
465		470		475 480
Ile Gly Leu Val Pro His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val				
	485		490	495
Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys				
	500		505	510
Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro				
	515		520	525
Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala				
	530		535	540
Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys Cys Arg Glu				
545		550		555 560
Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg Asp				
	565		570	575
Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu				
	580		585	590
Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly Thr Val				
	595		600	605
His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys His Ala				
	610		615	620
Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser Asn Cys Lys				
625		630		635 640
Lys Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu Asn Val				
	645		650	655
Lys Gly Thr Glu Asp Ser Gly Thr Thr Val Leu Leu Pro Leu Val Ile				
	660		665	670
Phe Phe Gly Leu Cys Leu Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr				
	675		680	685
Arg Tyr Gln Arg Trp Lys Ser Asp Leu Tyr Ser Ile Val Cys Gly Lys				
	690		695	700
Ser Thr Pro Glu Lys Glu Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro				
705		710		715 720
Leu Ala Pro Asn Pro Ser Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr				
	725		730	735
Leu Gly Phe Ser Pro Val Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr				
	740		745	750

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Tyr Thr Pro Gly Asp Cys Pro Asn Phe Ala Ala Pro Arg Arg Glu Val  
 755 760 765  
 Ala Pro Pro Tyr Gln Gly Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala  
 770 775 780  
 Ser Asp Pro Ile Pro Asn Pro Leu Gln Lys Trp Glu Asp Ser Ala His  
 785 790 795 800  
 Lys Pro Gln Ser Leu Asp Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val  
 805 810 815  
 Val Glu Asn Val Pro Pro Leu Arg Trp Lys Glu Phe Val Arg Arg Leu  
 820 825 830  
 Gly Leu Ser Pro His Glu Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg  
 835 840 845  
 Cys Leu Arg Glu Ala Gln Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg  
 850 855 860  
 Thr Pro Arg Arg Glu Ala Thr Leu Glu Leu Leu Gly Arg Val Leu Arg  
 865 870 875 880  
 Asp Met Asp Leu Leu Gly Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys  
 885 890 895  
 Gly Pro Ala Ala Leu Pro Pro Ala Pro Ser Leu Leu Arg  
 900 905

## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Glu Gln Arg Pro Arg Gly Cys Ala Ala Val Ala Ala Ala Leu Leu  
 1 5 10 15  
 Leu Val Leu Leu Gly Ala Arg Ala Gln Gly Gly Thr Arg Ser Pro Arg  
 20 25 30  
 Cys Asp Cys Ala Gly Asp Phe His Lys Lys Ile Gly Leu Phe Cys Cys  
 35 40 45

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Sub  
 App  
 cont.

Arg Gly Cys Pro Ala Gly His Tyr Leu Lys Ala Pro Cys Thr Glu Pro  
 50 55 60  
 Cys Gly Asn Ser Thr Cys Leu Val Cys Pro Gln Asp Thr Phe Leu Ala  
 65 70 75 80  
 Trp Glu Asn His His Asn Ser Glu Cys Ala Arg Cys Gln Ala Cys Asp  
 85 90 95  
 Glu Gln Ala Ser Gln Val Ala Leu Glu Asn Cys Ser Ala Val Ala Asp  
 100 105 110  
 Thr Arg Cys Gly Cys Lys Pro Gly Trp Phe Val Glu Cys Gln Val Ser  
 115 120 125  
 Gln Cys Val Ser Ser Ser Pro Phe Tyr Cys Gln Pro Cys Leu Asp Cys  
 130 135 140  
 Gly Ala Leu His Arg His Thr Arg Leu Leu Cys Ser Arg Arg Asp Thr  
 145 150 155 160  
 Asp Cys Gly Thr Cys Leu Pro Gly Phe Tyr Glu His Gly Asp Gly Cys  
 165 170 175  
 Val Ser Cys Pro Thr Ser Thr Leu Gly Ser Cys Pro Glu Arg Cys Ala  
 180 185 190  
 Ala Val Cys Gly Trp Arg Gln Met Phe Trp Val Gln Val Leu Leu Ala  
 195 200 205  
 Gly Leu Val Val Pro Leu Leu Leu Gly Ala Thr Leu Thr Tyr Thr Tyr  
 210 215 220  
 Arg His Cys Trp Pro His Lys Pro Leu Val Thr Ala Asp Glu Ala Gly  
 225 230 235 240  
 Met Glu Ala Leu Thr Pro Pro Pro Ala Thr His Leu Ser Pro Leu Asp  
 245 250 255  
 Ser Ala His Thr Leu Leu Ala Pro Pro Asp Ser Ser Glu Lys Ile Cys  
 260 265 270  
 Thr Val Gln Leu Val Gly Asn Ser Trp Thr Pro Gly Tyr Pro Glu Thr  
 275 280 285  
 Gln Glu Ala Leu Cys Pro Gln Val Thr Trp Ser Trp Asp Gln Leu Pro  
 290 295 300  
 Ser Arg Ala Leu Gly Pro Ala Ala Ala Pro Thr Leu Ser Pro Glu Ser  
 305 310 315 320  
 Pro Ala Gly Ser Pro Ala Met Met Leu Gln Pro Gly Pro Gln Leu Tyr  
 325 330 335  
 Asp Val Met Asp Ala Val Pro Ala Arg Arg Trp Lys Glu Phe Val Arg

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Sub  
Ala  
Cont

350

Sub  
A6  
cent

Arg His Cys Trp Pro His Lys Pro Leu Val Thr Ala Asp Glu Ala Gly  
 645 650 655  
 Met Glu Ala Leu Thr Pro Pro Pro Ala Thr His Leu Ser Pro Leu Asp  
 660 665 670  
 Ser Ala His Thr Leu Leu Ala Pro Pro Asp Ser Ser Glu Lys Ile Cys  
 675 680 685  
 Thr Val Gln Leu Val Gly Asn Ser Trp Thr Pro Gly Tyr Pro Glu Thr  
 690 695 700  
 Gln Glu Ala Leu Cys Pro Gln Val Thr Trp Ser Trp Asp Gln Leu Pro  
 705 710 715 720  
 Ser Arg Ala Leu Gly Pro Ala Ala Ala Pro Thr Leu Ser Pro Glu Ser  
 725 730 735  
 Pro Ala Gly Ser Pro Ala Met Met Leu Gln Pro Gly Pro Gln Leu Tyr  
 740 745 750  
 Asp Val Met Asp Ala Val Pro Ala Arg Arg Trp Lys Glu Phe Val Arg  
 755 760 765  
 Thr Leu Gly Leu Arg Glu Ala Glu Ile Glu Ala Val Glu Val Glu Ile  
 770 775 780  
 Gly Arg Phe Arg Asp Gln Gln Tyr Glu Met Leu Lys Arg Trp Arg Gln  
 785 790 795 800  
 Gln Gln Pro Ala Gly Leu Gly Ala Val Tyr Ala Ala Leu Glu Arg Met  
 805 810 815  
 Gly Leu Asp Gly Cys Val Glu Asp Leu Arg Ser Arg Leu Gln Arg Gly  
 820 825 830  
 Pro

00013895.012793

Sub  
Ala  
Cys

## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGCANAGGTN CGTACCTAGC TCACCTGCAA CCATCAAAC T NATGATCAA TCAATTGGCA 60  
CACAGCAATG GGAAACATAG CCCTTTGGAA GANTTGTNTC CACCAGGATC TCATAGATCA 120  
AAACATCCTG GGAGCCTGTT AACCGGTGCC CCAAAGGNTG GTCAAGGTCA AGGAATTGTT 180  
NCGCCCTGGA AGTGAACATC GAGTGTNTCC ACAAAGGATT CAGGCAATGG GACATAAATA 240  
TATGGGTGAA TTTTGGTTGT GAACTTTGGT TGNTCCCGTT GNTGTTGNTG GCTGTGCTGA 300  
TTGTTTGTG TTGCATCGGC TTCAGGTTNT GGAGGGGGAC CCAAGTGCAT GGACAGGGTG 360  
TGTTTCTGGG GTTTGGGTCT CTTAGAGGGC NTGGGT TANG GCANGTTCAC AAGGGTTTTA 420  
GCAANG 426

## (2) INFORMATION FOR SEQ ID NO:7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TGGGGCTGAG GACAATGCTG ACNACGAGAT TCTGAGCAAC GCAGNACTNG CTGTCCACTT 60  
TCGTCTNTGN GCAGCAAATG GAAAGCCAGG AGCCGGCAGA TTTGACAGGT GTCAGTGTAC 120  
AGTCCCCAGG GGAGGCACAG TGTCTGCTGG TGAGTTGGGG ACAGGCCCTT GCAAGACCTT 180  
GTGAGGCAGG GGGTGAAGGC CATGNCTCGG CTTCNNNTGG TCAAAGGGGA AGTGGAGCCT 240  
GAGGGAGATG GGA CTTNAGG GGGACGGNGC TGCGTGGGGA AAAAGCAGCC ACCNTTTGAC 300  
AAGGGGGACA GGCATTTTTN CAAATGTGTG CTTNTTGGT 339

09013895.012798

Sub  
a6  
cont.



## (2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCGGCATGCA TGATCAATCA ATTGGCAC

28

## (2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCGGGATCCG CCATCATGGC GCCACCACCA GCTAGA

36

## (2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GCGGGATCCT CACTCCAAGG ACACGGCAGA GCG

33

## (2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GCGGGATCCT CAATTATGTC CATTGCCTG

29

0123456789101112131415161718192021222324252627282930313233343536373839404142434445464748495051525354555657585960616263646566676869707172737475767778798081828384858687888990919293949596979899100101102103104105106107108109110111112113114115116117118119120121122123124125126127128129130131132133134135136137138139140141142143144145146147148149150151152153154155156157158159160161162163164165166167168169170171172173174175176177178179180181182183184185186187188189190191192193194195196197198199200201202203204205206207208209210211212213214215216217218219220221222223224225226227228229230231232233234235236237238239240241242243244245246247248249250251252253254255256257258259260261262263264265266267268269270271272273274275276277278279280281282283284285286287288289290291292293294295296297298299300301302303304305306307308309310311312313314315316317318319320321322323324325326327328329330331332333334335336337338339340341342343344345346347348349350351352353354355356357358359360361362363364365366367368369370371372373374375376377378379380381382383384385386387388389390391392393394395396397398399400401402403404405406407408409410411412413414415416417418419420421422423424425426427428429430431432433434435436437438439440441442443444445446447448449450451452453454455456457458459460461462463464465466467468469470471472473474475476477478479480481482483484485486487488489490491492493494495496497498499500501502503504505506507508509510511512513514515516517518519520521522523524525526527528529530531532533534535536537538539540541542543544545546547548549550551552553554555556557558559560561562563564565566567568569570571572573574575576577578579580581582583584585586587588589590591592593594595596597598599600601602603604605606607608609610611612613614615616617618619620621622623624625626627628629630631632633634635636637638639640641642643644645646647648649650651652653654655656657658659660661662663664665666667668669670671672673674675676677678679680681682683684685686687688689690691692693694695696697698699700701702703704705706707708709710711712713714715716717718719720721722723724725726727728729730731732733734735736737738739740741742743744745746747748749750751752753754755756757758759760761762763764765766767768769770771772773774775776777778779780781782783784785786787788789790791792793794795796797798799800801802803804805806807808809810811812813814815816817818819820821822823824825826827828829830831832833834835836837838839840841842843844845846847848849850851852853854855856857858859860861862863864865866867868869870871872873874875876877878879880881882883884885886887888889890891892893894895896897898899900901902903904905906907908909910911912913914915916917918919920921922923924925926927928929930931932933934935936937938939940941942943944945946947948949950951952953954955956957958959960961962963964965966967968969970971972973974975976977978979980981982983984985986987988989990991992993994995996997998999100010011002100310041005100610071008100910101011101210131014101510161017101810191020102110221023102410251026102710281029103010311032103310341035103610371038103910401041104210431044104510461047104810491050105110521053105410551056105710581059106010611062106310641065106610671068106910701071107210731074107510761077107810791080108110821083108410851086108710881089109010911092109310941095109610971098109911001101110211031104110511061107110811091110111111121113111411151116111711181119112011211122112311241125112611271128112911301131113211331134113511361137113811391140114111421143114411451146114711481149115011511152115311541155115611571158115911601161116211631164116511661167116811691170117111721173117411751176117711781179118011811182118311841185118611871188118911901191119211931194119511961197119811991200120112021203120412051206120712081209121012111212121312141215121612171218121912201221122212231224122512261227122812291230123112321233123412351236123712381239124012411242124312441245124612471248124912501251125212531254125512561257125812591260126112621263126412651266126712681269127012711272127312741275127612771278127912801281128212831284128512861287128812891290129112921293129412951296129712981299130013011302130313041305130613071308130913101311131213131314131513161317131813191320132113221323132413251326132713281329133013311332133313341335133613371338133913401341134213431344134513461347134813491350135113521353135413551356135713581359136013611362136313641365136613671368136913701371137213731374137513761377137813791380138113821383138413851386138713881389139013911392139313941395139613971398139914001401140214031404140514061407140814091410141114121413141414151416141714181419142014211422142314241425142614271428142914301431143214331434143514361437143814391440144114421443144414451446144714481449145014511452145314541455145614571458145914601461146214631464146514661467146814691470147114721473147414751476147714781479148014811482148314841485148614871488148914901491149214931494149514961497149814991500150115021503150415051506150715081509151015111512151315141515151615171518151915201521152215231524152515261527152815291530153115321533153415351536153715381539154015411542154315441545154615471548154915501551155215531554155515561557155815591560156115621563156415651566156715681569157015711572157315741575157615771578157915801581158215831584158515861587158815891590159115921593159415951596159715981599160016011602160316041605160616071608160916101611161216131614161516161617161816191620162116221623162416251626162716281629163016311632163316341635163616371638163916401641164216431644164516461647164816491650165116521653165416551656165716581659166016611662166316641665166616671668166916701671167216731674167516761677167816791680168116821683168416851686168716881689169016911692169316941695169616971698169917001701170217031704170517061707170817091710171117121713171417151716171717181719172017211722172317241725172617271728172917301731173217331734173517361737173817391740174117421743174417451746174717481749175017511752175317541755175617571758175917601761176217631764176517661767176817691770177117721773177417751776177717781779178017811782178317841785178617871788178917901791179217931794179517961797179817991800180118021803180418051806180718081809181018111812181318141815181618171818181918201821182218231824182518261827182818291830183118321833183418351836183718381839184018411842184318441845184618471848184918501851185218531854185518561857185818591860186118621863186418651866186718681869187018711872187318741875187618771878187918801881188218831884188518861887188818891890189118921893189418951896189718981899190019011902190319041905190619071908190919101911191219131914191519161917191819191920192119221923192419251926192719281929193019311932193319341935193619371938193919401941194219431944194519461947194819491950195119521953195419551956195719581959196019611962196319641965196619671968196919701971197219731974197519761977197819791980198119821983198419851986198719881989199019911992199319941995199619971998199920002001200220032004200520062007200820092010201120122013201420152016201720182019202020212022202320242025202620272028202920302031203220332034203520362037203820392040204120422043204420452046204720482049205020512052205320542055205620572058205920602061206220632064206520662067206820692070207120722073207420752076207720782079208020812082208320842085208620872088208920902091209220932094209520962097209820992100210121022103210421052106210721082109211021112112211321142115211621172118211921202121212221232124212521262127212821292130213121322133213421352136213721382139214021412142214321442145214621472148214921502151215221532154215521562157215821592160216121622163216421652166216721682169217021712172217321742175217621772178217921802181218221832184218521862187218821892190219121922193219421952196219721982199220022012202220322042205220622072208220922102211221222132214221522162217221822192220222122222223222422252226222722282229223022312232223322342235223622372238223922402241224222432244224522462247224822492250225122522253225422552256225722582259226022612262226322642265226622672268226922702271227222732274227522762277227822792280228122822283228422852286228722882289229022912292229322942295229622972298229923002301230223032304230523062307230823092310231123122313231423152316231723182319232023212322232323242325232623272328232923302331233223332334233523362337233823392340234123422343234423452346234723482349235023512352235323542355235623572358235923602361236223632364236523662367236823692370237123722373237423752376237723782379238023812382238323842385238623872388238923902391239223932394239523962397239823992400240124022403240424052406240724082409241024112412241324142415241624172418241924202421242224232424242524262427242824292430243124322433243424352436243724382439244024412442244324442445244624472448244924502451245224532454245524562457245824592460246124622463246424652466246724682469247024712472247324742475247624772478247924802481248224832484248524862487248824892490249124922493249424952496249724982499250025012502250325042505250625072508250925102511251225132514251525162517251825192520252125222523252425252526252725282529253025312532253325342535253625372538253925402541254225432544254525462547254825492550255125522553255425552556255725582559256025612562256325642565256625672568256925702571257225732574257525762577257825792580258125822583258425852586258725882589259025912592259325942595259625972598259926002601260226032604260526062607260826092610261126122613261426152616261726182619262026212622262326242625262626272628262926302631263226332634263526362637263826392640264126422643264426452646264726482649265026512652265326542655265626572658265926602661266226632664266526662667266826692670267126722673267426752676267726782679268026812682268326842685268626872688268926902691269226932694269526962697269826992700270127022703270427052706270727082709271027112712271327142715271627172718271927202721272227232724272527262727272827292730273127322733273427352736273727382739274027412742274327442745274627472748274927502751275227532754275527562757275827592760276127622763276427652766276727682769277027712772277327742775277627772778277927802781278227832784278527862787278827892790279127922793279427952796279727982799280028012802280328042805280628072808280928102811281228132814281528162817281828192820282128222823282428252826282728282829283028312832283328342835283628372838283928402841284228432844284528462847284828492850285128522853285428552856285728582859286028612862286328642865286628672868286928702871287228732874287528762877287828792880288128822883288428852886288728882889289028912892289328942895289628972898289929002901290229032904290529062907290829092910291129122913291429152916291729182919292029212922292329242925292629272928292929302931293229332934293529362937293829392940294129422943294429452946294729482949295029512952295329542955295629572958295929602961296229632964296529662967296829692970297129722973297429752976297729782979298029812982298329842985298629872988298929902991299229932994299529962997299829993000300130023003300430053006300730083009301030113012301330143015301630173018